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| EXAMINER | |
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| RIGGS II, LARRY D | |

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**Please find below and/or attached an Office communication concerning this application or proceeding.**

The time period for reply, if any, is set in the attached communication.

| Office Action Summary | Application No. | Applicant(s) | |
|---|---|---|---|
| | 10/632,099 | CHEN ET AL. | |
| | Examiner | Art Unit | |
| | Larry D. Riggs II | 1631 | |

*-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --*

**Period for Reply**

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

**Status**

1)☐ Responsive to communication(s) filed on *19 October 2007*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

**Disposition of Claims**

4)☒ Claim(s) *1-62* is/are pending in the application.

4a) Of the above claim(s) *33-57 and 59-62* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-32 and 58* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

**Application Papers**

9)☒ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *01 August 2003* is/are: a)☒ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☒ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

**Priority under 35 U.S.C. § 119**

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

**Attachment(s)**

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date *10 June 2005*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

## DETAILED ACTION

### *Election/Restrictions*

It is noted that there is no claim 25 in the originally filed claims or in the amended claims filed 10/19/07. Pursuant to 37 CFR 1.75(f), claims 26-62 have been renumbered as claims 25-61, respectively. A claim listing with the corrected claim numbers has been scanned into the IFW file of the application concurrent with the present Office action. Consequently, the claims encompassed in the invention of Group I set forth in the restriction requirement mailed 9/20/07 should include claims 1-31 and 57.

Applicant's election without traverse of Group I (claims 1-31 and 57), drawn to a method of identifying a drug discovery target, in the reply filed on 19 October 2007 is acknowledged.

Claims 32-56 and 58-61 are withdrawn from further consideration pursuant to 37 CFR 1.142(b) as being drawn to a nonelected invention, there being no allowable generic or linking claim. Election was made **without** traverse in the reply filed on 19 October 2007.

### *Oath/Declaration*

The oath or declaration is defective. A new oath or declaration in compliance with 37 CFR 1.67(a) identifying this application by application number and filing date is required. See MPEP §§ 602.01 and 602.02.

The oath or declaration is defective because:

Non-initialed and/or non-dated alterations have been made to the oath or declaration. See 37 CFR 1.52(c).

In the instant case, the post office address of inventor Keith Steward was changed, but the alternation was not initialed and dated. See page 10, 15, 19 of the amended oath filed 09 January 2007.

***Specification***

The disclosure is objected to because it contains an embedded hyperlink and/or other form of browser-executable code, (see specification, page 29, paragraph 90). Applicant is required to delete the embedded hyperlink and/or other form of browser-executable code. See MPEP § 608.01.

The uses of the trademarks such as BIOSIS, GENBANK and AFFYMETRIX GENECHIP, have been noted in this application. They can be found, for example, in paragraphs 9, 10 and 74, of the specification. Trademarks should be capitalized wherever they appear and be accompanied by the generic terminology.

Although the use of trademarks is permissible in patent applications, the proprietary nature of the marks should be respected and every effort made to prevent their use in any manner which might adversely affect their validity as trademarks.

Appropriate correction is required.

### *Claim Objection, Warning*

Applicant is advised that should claim 5 be found allowable, claim 6 will be objected to under 37 C.F.R. 1.75 as being a substantial duplicate thereof. When two claims in an application are duplicates or else are so close in content that they both cover the same thing, despite a slight difference in wording, it is proper after allowing one claim to object to the other as being a substantial duplicate of the allowed claim. See MPEP § 706.03(k). In the instant case, claims 5 and 6 are identical.

Claim 25 is objected to because of the following informality:

The limitation "a microarray experiments a prior analysis" is grammatically incorrect. It is suggested that re-wording the claim as "a microarray experiment, a prior analysis" would suffice.

Appropriate correction is required.

### *Claim Rejections - 35 USC § 112*

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 1-31 and 57 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claim 1 in line 7 and claim 57 in line 4, recites the limitation "each such reaction". There is insufficient antecedent basis for this limitation in the claim. There is no prior reference to a reaction.

Claim 1 recites the limitation "the stored concepts" in line 3. There is insufficient antecedent basis for this limitation in the claim. There is no prior reference to any stored concepts.

Claim 2 recites the limitation "the proteins that result", line 2. The metes and bounds of the limitation are unclear. It is suggested that re-wording of the claim such as "proteins expressed from said genes" would suffice in clarification of the limitation.

Claim 3 in line 1, claim 4 in line 1, claim 5 in line 1 and claim 6 in line 1, recites the limitation "the data". There is insufficient antecedent basis for this limitation in the claim. There is no prior reference to the limitation.

Claim 8 in line 1 and claim 9 in line 1, recites the limitation "the candidate drug discovery targets". This limitation lacks clear antecedent basis because there is no prior reference to a candidate drug discovery target in claim 2 or 1.

Claim 10 recites the limitation "the results of additional data", line 2. It is unclear what is meant by the limitation.

Claim 11 recites the limitation "the method of claim 10" in line 1. The limitation lacks clear antecedent basis because there are different "methods" recited in claim 10, such as the method in line 1 and the "additional methods" in line 2. Thus, it is not clear which method is referred to in claim 11.

Claim 13 in line 2 and claim 14 in line 2, recites the limitation "gene product". The metes and bound of the limitation are unclear as to whether the limitation refers to RNA, protein or both.

Claim 14 recites the limitation "relationships that are at least one step removed" in line 3. It is unclear what the metes and bounds of the limitation are because there has been no prior reference as to what the relationships would be removed from or how one skilled in the art could determine what specifically comprises said relationships to distinguish them by said step.

Claim 18 recites the limitation "relevant findings" in line 2. It is unclear how one skilled in the art would distinguish relevant from irrelevant findings.

Claim 19 recites the limitation "statistically significant". The metes and bound of the limitation are unclear because neither the instant claim, claim 18, claim 1 or the specification defines what would be statistically significant.

Claim 24 in lines 2 and 3, recites the limitation "the data". There is insufficient antecedent basis for this limitation in the claim. There is no prior reference to the limitation in claim 20 or in claim 1.

Claim 24 in lines 2 and 3, recites the limitation "the user-supplied genomics data". There is insufficient antecedent basis for this limitation in the claim. There is no prior reference to the limitation in claim 20 or in claim 1.

Claim 29 recites the limitation "a first known drug target gene and a second gene of interest" in line 2. It is unclear whether the "second gene" referred to in the limitation is actually a drug target gene or a different category of gene.

Claim 30 recites the limitation "derived about a central biological process for all process in the database" in line 2. The metes and bound of the limitation are unclear as to what other processes in the database applicant refers and how one skilled in the art

could distinguish said central biological process from other processes since only genomics information is only be analyzed in the instant invention.

Claim 31 recites the limitation "structure centric" in line 2. The metes and bound of the limitation are unclear as to what structure applicant is referring, such as a chemical structure, protein structure, etc.

Claim 31 recites the limitation "structure centric" in line 2. The metes and bound of the limitation are unclear as to what other objects in the database applicant refers and how one skilled in the art could distinguish said central physical object from other objects in the database.

***Claim Rejections - 35 USC § 101***

35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

Claims 1-31 and 57 are rejected under 35 U.S.C. 101 because the claimed invention is directed to non-statutory subject matter.

The instant invention is drawn to a method for identifying a drug discovery target which comprises providing a means for accessing genomics information in a database wherein said means permits computational analysis of biological relationships among the stored concepts, generating one or more subsets of genomics information from the database wherein at least one of the one or more subsets is a disease-related pathway, and identifying the biological interactions and actor concepts in the disease-related

pathway whereby each of the actor concepts involved in each such reaction is a drug discovery target.

In the instant claims, there is no physical transformation by the claimed invention, thus the Examiner must determine if the instant claims produce a useful, tangible, and concrete final result.

In determining if the instant claims have a useful, tangible, and concrete final result, the Examiner must determine each standard individually. For a claim to be "useful", the claim must produce a final result that is specific, substantial and credible. For a claim to be "tangible", the claim must set forth a practical application of the invention that produces a real-world final result. For a claim to be "concrete", the process must have a final result that can be substantially repeatable or the process must substantially produce the same result again. Furthermore, the claim must recite a useful, tangible, and concrete final result in the claim itself, and the claim must be limited only to statutory embodiments. Thus if the claim is broader than the statutory embodiments of the claim, the Examiner must reject the claim as non-statutory.

The instant claims do not produce a tangible final result. A tangible requirement requires that the claim must set forth a practical application of the analysis of the genomics information in the database to produce a real-world result. The instant claims are drawn to a method of identifying the biological interactions and actor concepts in a disease-related pathway obtained from genomics information from a database. However, the last step of the claims include identifying a drug discovery target obtained from the analysis of the data from the database, the result of the invention is a point of

data, such as a drug target from the analysis of data, which, in itself, are not tangible. Since the claim itself must include a useful, concrete and tangible final result, the instant claims are non-statutory.

This rejection could be overcome by amendment of the claims to recite that a specific final result of the process is outputted to a user, or by including a result that is a physical transformation. The applicants are cautioned against introduction of new matter in an amendment.

***Claim Rejections - 35 USC § 102***

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 1-15, 18-27, 29-31 and 57 are rejected under 35 U.S.C. 102(b) as being anticipated by Qu et al.

In view of the indefiniteness of the claims as set forth above, the art is being applied to the best interpretation of the claims as written.

The instant claims are drawn to a method of identifying disease-related pathways that can be used to identify drug discovery targets.

Regarding claim 1, Qu et al. teaches a bioinformatics system that performs multidimensional data analysis to discover gene functions and uses cluster analysis to infer gene relationships to discover drug targets. Qu et al. shows accessing genomics

information through data warehousing, (see page 21, right column; page 22, left and middle columns), generating subsets of information that are disease-related pathways through data integration, (see page 22, middle and right columns; pages 25-26, Figure 4) and identifying genes and molecules that may be drug target candidates, (see page 21, right column, last paragraph; Figure 1).

Regarding claim 2, Qu et al. shows a data mart that is a multi-dimensional database encompassing information from genes to the biological effects of their expressed proteins, (see page 23 – page 24, middle column).

Regarding claim 3, Qu et al. shows data extracted from multiple public sources such as the Institute for Genome Research, Sanger Center, National Cancer Institute and literature, (see page 24, left column; Figure 1).

Regarding claim 4, Qu et al. shows data obtained from "in house" assays, (see page 22, middle and right columns).

Regarding claims 5 and 6, Qu et al. shows data obtained from multiple public sources such as the Institute for Genome Research, Sanger Center, National Cancer Institute and literature, (see page 24, left column; Figure 1) and from "in house" assays, (see page 22, middle and right columns).

Regarding claim 7, the specification defines slots and facets as to define and structure the taxonomic relationship between classes or groups of things that share similar properties, (see specification, page 9, paragraphs 40 and 41). Qu et al. shows ontology vocabulary mapping which provides a formal written description of a specific set of concepts and their relationships in a particular domain based on Stanford

University's Gene Ontology Consortium for categorizing molecular function, biological process and cellular components, (see page 22, right column – page 23, left column).

Regarding claim 8, Qu et al. shows functional assays to screen for genes that have important functions in a disease pathway before knowing the genes identities, like cell-cycle functional screening assays and complex protein-protein interactions with several hundred proteins involved in the pathways of interest to elucidate a drug discovery target, (see page 22, middle and right columns; page 25 – page 26; Figure 4).

Regarding claim 9, Qu et al. shows that after specificity and activity of the optimized lead compounds, their drug effects are further characterized in animal models and preclinical studies, (see page 22, left column).

Regarding claim 10, Qu et al. shows that after using YTH binding relationships as the core matrix of data analysis, the possibility of integrating additional heterogeneous data for more specific and accurate pathway inference for target analysis, (see page 24, middle column – page 25, middle column).

Regarding claim 11, Qu et al. shows obtaining data from protein-protein interaction studies and profiling with mass spectrometry, (see page 21, right column; page 22, right column; Figure 1).

Regarding claim 12, Qu et al. shows obtaining data from gene expression studies, (see page 22, colored text table); page 23, right column; Figure 1).

Regarding claim 13, Qu et al. shows incorporating multiple genomes as data sources for the operational relational database, (see page 24, left column; Figure 1).

Regarding claim 14, Qu et al. shows accessing genomics information through data warehousing, (see page 21, right column; page 22, left and middle columns), generating subsets of information that are disease-related pathways through data integration, (see page 22, middle and right columns; pages 25-26, Figure 4) and identifying genes and molecules that may be drug target candidates, (see page 21, right column, last paragraph; Figure 1), such as genes identified from clustering analysis based on YTH and domain data and their biological effects, (see page 25 – page 26, Figures 5 and 6).

Regarding claim 15, Qu et al. shows comparing database data with user defined data, (see page 22, left and middle columns), and using a relationship inference model, (see page 24 – page 25).

Regarding claim 18, Qu et al. shows utilizing ontology to classify relevant genes or cellular components associated with a pathway, (see page 22, right column – page 23, left column).

Regarding claim 19, Qu et al. shows classifying statistically significant hits for a query protein, (see page 23, right column).

Regarding claim 20, the specification defines profile that may include information about and be defined according to concepts such as a particular combination of genes or gene products that appear to a act in a biologically coordinated manner, (see paragraph 75). Qu et al. shows generating clusters of a characteristic matrix where groups of proteins which have similar functions or participate in the same pathway, (see page 24, middle column - page 25, middle column).

Regarding claims 21 and 22, Qu et al. shows clustering from a database and user provided data with an extension of the data warehouse with data from analysis with a model driven approach, (see page 22, middle and right columns; page 24, middle column - page 25, middle column; Equations 1 and 2.)

Regarding claims 23 and 24, Qu et al. shows cluster from database data and data supplied by user analysis with an extension of the data warehouse with data from analysis, (page 22, middle column – page 23, right column).

Regarding claim 25, Qu et al. shows data used for clustering may include user supplied gene expression data from microarrays experiments and query sequences, (see page 23, middle and right columns).

Regarding claim 26, Qu et al. shows gene-centric analysis of the data warehouse, (see page 22, left column).

Regarding claim 27, Qu et al. shows developing clusters with related genes as a training set for a relationship inference model, (see page 26, right column).

Regarding claim 29, Qu et al. shows using known bait genes or proteins to identify their interacting partners as a potential drug target, (see Figure 1, page 21, right column; page 24, middle and right columns).

Regarding claim 30, Qu et al. shows clusters with common function and process, (see page 25, left – right columns).

Regarding claim 31, Qu et al. shows matrixes with structures used as templates defining families of structurally similar proteins, (see page 23, left – right columns).

Regarding claim 57, Qu et al. shows computer system allowing the accessing of genomics information through data warehousing, (see page 21, right column; page 22, left and middle columns), generating subsets of information that are disease-related pathways through data integration, (see page 22, middle and right columns; pages 25-26, Figure 4) and identifying genes and molecules that may be drug target candidates, (see page 21, right column, last paragraph; Figure 1).

### *Claim Rejections - 35 USC § 103*

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

The factual inquiries set forth in *Graham* **v.** *John Deere Co.*, 383 U.S. 1, 148 USPQ 459 (1966), that are applied for establishing a background for determining obviousness under 35 U.S.C. 103(a) are summarized as follows:

1. Determining the scope and contents of the prior art.
2. Ascertaining the differences between the prior art and the claims at issue.
3. Resolving the level of ordinary skill in the pertinent art.
4. Considering objective evidence present in the application indicating obviousness or nonobviousness.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation

under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

Claims 16-17 and 28 are rejected under 35 USC 103(a) as being unpatentable over Qu et al., as applied to claims 1-15, 18-27, 29-31 and 57 above, further in view of Bura et al.

The instant claims are drawn to a method of identifying disease-related pathways than can be used to identify drug discovery targets. Regarding claims 16, 17 and 28, the instant claims are drawn to a method for identifying a drug discovery target which comprises providing a means for accessing genomics information in a database wherein said means permits computational analysis of biological relationships among the stored concepts, generating one or more subsets of genomics information from the database wherein at least on of the one or more subsets is a disease-related pathway, and identifying the biological interactions and actor concepts in the disease-related pathway whereby each of the actor concepts involved in each such reaction is a drug discovery target, wherein the comparing step includes identifying an overlap between user-defined data and data form the database and the statistical model is a statistical significance model measuring the likelihood that the overlap is a random event, wherein the user defined data is one of gene expression data and manually entered gene list, and the profiles, generated as a subset of genomics information, are generated so as to

be non-overlapping by ensuring that user-selected genes do not appear in more than a predetermined maximum threshold number of generated profiles.

Qu et al. is applied as to claims 1-15, 18-27, 29-31 and 57 above.

However, Qu et al. does not show identifying an overlap between data sets and measuring the likelihood that the overlap is a random event.

Bura et al. shows a binary regression quantile plot and area defined by it used for visual comparison and ordering of nested binary response regression models.

Bura et al. also shows total gain model and measure binary regression quantile plots for simulated data with various degrees of overlap, wherein they are ordered with the best corresponding to minimum overlap and the worst corresponding to almost random overlap, (see page 8, last paragraph; Equation 5; page 10, paragraph 2; Figure 2).

It would have been obvious to one of ordinary skill in the art at the time of the instant invention to modify the bioinformatics system that performs multidimensional data analysis to discover gene functions and uses cluster analysis to infer gene relationships to discover drug targets of Qu et al. with the total gain model by Bura et al. because by Qu et al. uses cluster analysis that seeks to organize information about variables to form relatively homogeneous groups, (see page 24, right column).

***Double Patenting***

The nonstatutory double patenting rejection is based on a judicially created doctrine grounded in public policy (a policy reflected in the statute) so as to prevent the unjustified or improper timewise extension of the "right to exclude" granted by a patent and to prevent possible harassment by multiple assignees. A nonstatutory

obviousness-type double patenting rejection is appropriate where the conflicting claims are not identical, but at least one examined application claim is not patentably distinct from the reference claim(s) because the examined application claim is either anticipated by, or would have been obvious over, the reference claim(s). See, e.g., *In re Berg*, 140 F.3d 1428, 46 USPQ2d 1226 (Fed. Cir. 1998); *In re Goodman*, 11 F.3d 1046, 29 USPQ2d 2010 (Fed. Cir. 1993); *In re Longi*, 759 F.2d 887, 225 USPQ 645 (Fed. Cir. 1985); *In re Van Ornum*, 686 F.2d 937, 214 USPQ 761 (CCPA 1982); *In re Vogel*, 422 F.2d 438, 164 USPQ 619 (CCPA 1970); and *In re Thorington*, 418 F.2d 528, 163 USPQ 644 (CCPA 1969).

A timely filed terminal disclaimer in compliance with 37 CFR 1.321(c) or 1.321(d) may be used to overcome an actual or provisional rejection based on a nonstatutory double patenting ground provided the conflicting application or patent either is shown to be commonly owned with this application, or claims an invention made as a result of activities undertaken within the scope of a joint research agreement.

Effective January 1, 1994, a registered attorney or agent of record may sign a terminal disclaimer. A terminal disclaimer signed by the assignee must fully comply with 37 CFR 3.73(b).

Claims 1-22, 26, 30 and 31 are provisionally rejected on the ground of nonstatutory obviousness-type double patenting as being unpatentable over claims 1-25 of copending Application No. 10/502420. Although the conflicting claims are not identical, they are not patentably distinct from each other because the claims of the copending application would anticipate the claims of the instant application. The only difference between claim 1 of the instant application and claim 1 of the copending application is that the instant claim 1 comprises "means for accessing genomics information in a database" whereas claim 1 of the copending application comprises "means for storing and accessing genomics information in a database." Clearly, claim 1 of the copending application teaches accessing genomics information in a database and thus anticipates the instant claim 1. Claims 2-22, 26, 30 and 31 of the instant application add similar limitations with only minor differences, to independent claim 1 of

the instant application, that claims 22-25 of the copending application add to claim 1 of the copending application.

This is a provisional obviousness-type double patenting rejection because the conflicting claims have not in fact been patented.

***Conclusion***

No claim allowed.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Larry D. Riggs II whose telephone number is 571-270-3062. The examiner can normally be reached on Monday-Thursday, 7:30AM-5:00PM, ALT. Friday, EST.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Marjorie Moran can be reached on 571-272-0720. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

/LDR/
Larry D. Riggs II
Examiner, Art Unit 1631

/Shubo (Joe) Zhou/
Shubo (Joe) Zhou, PH.D.
Primary Examiner